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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/076,416

DATE: 06/20/2002

TIME: 17:39:04

Input Set : A:\EP.txt

Output Set: N:\CRF3\06202002\J076416.raw

3 <110> APPLICANT: RIEPING, Mechthild  
 4 THIERBACH, Georg  
 6 <120> TITLE OF INVENTION: Process for the fermentative preparation of L-amino acids  
 using strains  
 7 of the Enterobacteriaceae family.  
 9 <130> FILE REFERENCE: 218162US0X  
 11 <140> CURRENT APPLICATION NUMBER: 10/076,416  
 12 <141> CURRENT FILING DATE: 2002-02-19  
 14 <150> PRIOR APPLICATION NUMBER: DE 10112107.5  
 15 <151> PRIOR FILING DATE: 2001-03-14  
 17 <150> PRIOR APPLICATION NUMBER: US 09/987541  
 18 <151> PRIOR FILING DATE: 2001-11-15  
 20 <150> PRIOR APPLICATION NUMBER: US 60/283612  
 21 <151> PRIOR FILING DATE: 2000-04-16  
 23 <150> PRIOR APPLICATION NUMBER: US 60/248210  
 24 <151> PRIOR FILING DATE: 2000-11-15  
 26 <160> NUMBER OF SEQ ID NOS: 12  
 28 <170> SOFTWARE: PatentIn version 3.1  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 1719  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Escherichia coli  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: CDS  
 37 <222> LOCATION: (1)..(1716)  
 38 <223> OTHER INFORMATION:  
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 44 1 5 10 15  
 46 ggg gtg aaa cgc atc tgg gga gtc aca ggc gac tct ctg aac ggt ctt 96  
 47 Gly Val Lys Arg Ile Trp Gly Val Thr Gly Asp Ser Leu Asn Gly Leu  
 48 20 25 30  
 50 agt gac agt ctt aat cgc atg ggc acc atc gag tgg atg tcc acc cgc 144  
 51 Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Glu Trp Met Ser Thr Arg  
 52 35 40 45  
 54 cac gaa gaa gtg gcg gcc ttt gcc gct ggc gct gaa gca caa ctt agc 192  
 55 His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Ser  
 56 50 55 60  
 58 gga gaa ctg gcg gtc tgc gcc gga tcg tgc ggc ccc ggc aac ctg cac 240  
 59 Gly Glu Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His  
 60 65 70 75 80  
 62 tta atc aac ggc ctg ttc gat tgc cac cgc aat cac gtt ccg gta ctg 288  
 63 Leu Ile Asn Gly Leu Phe Asp Cys His Arg Asn His Val Pro Val Leu

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64	85	90	95	
66 gcg att gcc gct cat att ccc tcc agc gaa att ggc agc ggc tat ttc				336
67 Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe				
68	100	105	110	
70 cag gaa acc cac cca caa gag cta ttc cgc gaa tgt agt cac tat tgc				384
71 Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys				
72	115	120	125	
74 gag ctg gtt tcc agc ccg gag cag atc cca caa gta ctg gcg att gcc				432
75 Glu Leu Val Ser Ser Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala				
76	130	135	140	
78 atg cgc aaa gcg gtg ctt aac cgt ggc gtt tcg gtt gtc gtg tta cca				480
79 Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro				
80 145	150	155	160	
82 ggc gac gtg gcg tta aaa cct gcg cca gaa ggg gca acc atg cac tgg				528
83 Gly Asp Val Ala Leu Lys Pro Ala Pro Glu Gly Ala Thr Met His Trp				
84	165	170	175	
86 tat cat gcg cca caa cca gtc gtg acg ccg gaa gaa gaa gag tta cgc				576
87 Tyr His Ala Pro Gln Pro Val Val Thr Pro Glu Glu Glu Glu Leu Arg				
88	180	185	190	
90 aaa ctg gcg caa ctg ctg cgt tat tcc agc aat atc gcc ctg atg tgt				624
91 Lys Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys				
92	195	200	205	
94 ggc agc ggc tgc gcg ggg gcg cat aaa gag tta gtt gag ttt gcc ggg				672
95 Gly Ser Gly Cys Ala Gly Ala His Lys Glu Leu Val Glu Phe Ala Gly				
96	210	215	220	
98 aaa att aaa gcg cct att gtt cat gcc ctg cgc ggt aaa gaa cat gtc				720
99 Lys Ile Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val				
100 225	230	235	240	
102 gaa tac gat aat ccg tat gat gtt gga atg acc ggg tta atc ggc ttc				768
103 Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe				
104	245	250	255	
106 tcg tca ggt ttc cat acc atg atg aac gcc gac acg tta gtg cta ctc				816
107 Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu				
108	260	265	270	
110 ggc acg caa ttt ccc tac cgc gcc ttc tac ccg acc gat gcc aaa atc				864
111 Gly Thr Gln Phe Pro Tyr Arg Ala Phe Tyr Pro Thr Asp Ala Lys Ile				
112	275	280	285	
114 att cag att gat atc aac cca gcc agc atc ggc gct cac agc aag gtg				912
115 Ile Gln Ile Asp Ile Asn Pro Ala Ser Ile Gly Ala His Ser Lys Val				
116	290	295	300	
118 gat atg gca ctg gtc ggc gat atc aag tcg act ctg cgt gca ttg ctt				960
119 Asp Met Ala Leu Val Gly Asp Ile Lys Ser Thr Leu Arg Ala Leu Leu				
120 305	310	315	320	
122 cca ttg gtg gaa gaa aaa gcc gat cgc aag ttt ctg gat aaa gcg ctg				1008
123 Pro Leu Val Glu Glu Lys Ala Asp Arg Lys Phe Leu Asp Lys Ala Leu				
124	325	330	335	
126 gaa gat tac cgc gac gcc cgc aaa ggg ctg gac gat tta gct aaa ccg				1056
127 Glu Asp Tyr Arg Asp Ala Arg Lys Gly Leu Asp Asp Leu Ala Lys Pro				
128	340	345	350	

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130 agc gag aaa gcc att cac ccg caa tat ctg gcg cag caa att agt cat      1104
131 Ser Glu Lys Ala Ile His Pro Gln Tyr Leu Ala Gln Gln Ile Ser His
132          355                      360                      365
134 ttt gcc gcc gat gac gct att ttc acc tgt gac gtt ggt acg cca acg      1152
135 Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr
136          370                      375                      380
138 gtg tgg gcg gca cgt tat cta aaa atg aac ggc aag cgt cgc ctg tta      1200
139 Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Lys Arg Arg Leu Leu
140 385                      390                      395                      400
142 ggt tcg ttt aac cac ggt tcg atg gct aac gcc atg ccg cag gcg ctg      1248
143 Gly Ser Phe Asn His Gly Ser Met Ala Asn Ala Met Pro Gln Ala Leu
144          405                      410                      415
146 ggt gcg cag gcg aca gag cca gaa cgt cag gtg gtc gcc atg tgc ggc      1296
147 Gly Ala Gln Ala Thr Glu Pro Glu Arg Gln Val Val Ala Met Cys Gly
148          420                      425                      430
150 gat ggc ggt ttt agc atg ttg atg ggc gat ttc ctc tca gta gtg cag      1344
151 Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Val Val Gln
152          435                      440                      445
154 atg aaa ctg cca gtg aaa att gtc gtc ttt aac aac agc gtg ctg ggc      1392
155 Met Lys Leu Pro Val Lys Ile Val Val Phe Asn Asn Ser Val Leu Gly
156          450                      455                      460
158 ttt gtg gcg atg gag atg aaa gct ggt ggc tat ttg act gac ggc acc      1440
159 Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr
160 465                      470                      475                      480
162 gaa cta cac gac aca aac ttt gcc cgc att gcc gaa gcg tgc ggc att      1488
163 Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile
164          485                      490                      495
166 acg ggt atc cgt gta gaa aaa gcg tct gaa gtt gat gaa gcc ctg caa      1536
167 Thr Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Glu Ala Leu Gln
168          500                      505                      510
170 cgc gcc ttc tcc atc gac ggt ccg gtg ttg gtg gat gtg gtg gtc gcc      1584
171 Arg Ala Phe Ser Ile Asp Gly Pro Val Leu Val Asp Val Val Val Ala
172          515                      520                      525
174 aaa gaa gag tta gcc att cca ccg cag atc aaa ctc gaa cag gcc aaa      1632
175 Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Glu Gln Ala Lys
176          530                      535                      540
178 ggt ttc agc ctg tat atg ctg cgc gca atc atc agc gga cgc ggt gat      1680
179 Gly Phe Ser Leu Tyr Met Leu Arg Ala Ile Ile Ser Gly Arg Gly Asp
180 545                      550                      555                      560
182 gaa gtg atc gaa ctg gcg aaa aca aac tgg cta agg taa      1719
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184          565                      570
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188 <211> LENGTH: 572
189 <212> TYPE: PRT
190 <213> ORGANISM: Escherichia coli
192 <400> SEQUENCE: 2
194 Met Lys Gln Thr Val Ala Ala Tyr Ile Ala Lys Thr Leu Glu Ser Ala
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198 Gly Val Lys Arg Ile Trp Gly Val Thr Gly Asp Ser Leu Asn Gly Leu
199          20          25          30
202 Ser Asp Ser Leu Asn Arg Met Gly Thr Ile Glu Trp Met Ser Thr Arg
203          35          40          45
206 His Glu Glu Val Ala Ala Phe Ala Ala Gly Ala Glu Ala Gln Leu Ser
207          50          55          60
210 Gly Glu Leu Ala Val Cys Ala Gly Ser Cys Gly Pro Gly Asn Leu His
211 65          70          75          80
214 Leu Ile Asn Gly Leu Phe Asp Cys His Arg Asn His Val Pro Val Leu
215          85          90          95
218 Ala Ile Ala Ala His Ile Pro Ser Ser Glu Ile Gly Ser Gly Tyr Phe
219          100         105         110
222 Gln Glu Thr His Pro Gln Glu Leu Phe Arg Glu Cys Ser His Tyr Cys
223          115         120         125
226 Glu Leu Val Ser Ser Pro Glu Gln Ile Pro Gln Val Leu Ala Ile Ala
227          130         135         140
230 Met Arg Lys Ala Val Leu Asn Arg Gly Val Ser Val Val Val Leu Pro
231 145         150         155         160
234 Gly Asp Val Ala Leu Lys Pro Ala Pro Glu Gly Ala Thr Met His Trp
235          165         170         175
238 Tyr His Ala Pro Gln Pro Val Val Thr Pro Glu Glu Glu Glu Leu Arg
239          180         185         190
242 Lys Leu Ala Gln Leu Leu Arg Tyr Ser Ser Asn Ile Ala Leu Met Cys
243          195         200         205
246 Gly Ser Gly Cys Ala Gly Ala His Lys Glu Leu Val Glu Phe Ala Gly
247          210         215         220
250 Lys Ile Lys Ala Pro Ile Val His Ala Leu Arg Gly Lys Glu His Val
251 225         230         235         240
254 Glu Tyr Asp Asn Pro Tyr Asp Val Gly Met Thr Gly Leu Ile Gly Phe
255          245         250         255
258 Ser Ser Gly Phe His Thr Met Met Asn Ala Asp Thr Leu Val Leu Leu
259          260         265         270
262 Gly Thr Gln Phe Pro Tyr Arg Ala Phe Tyr Pro Thr Asp Ala Lys Ile
263          275         280         285
266 Ile Gln Ile Asp Ile Asn Pro Ala Ser Ile Gly Ala His Ser Lys Val
267          290         295         300
270 Asp Met Ala Leu Val Gly Asp Ile Lys Ser Thr Leu Arg Ala Leu Leu
271 305         310         315         320
274 Pro Leu Val Glu Glu Lys Ala Asp Arg Lys Phe Leu Asp Lys Ala Leu
275          325         330         335
278 Glu Asp Tyr Arg Asp Ala Arg Lys Gly Leu Asp Asp Leu Ala Lys Pro
279          340         345         350
282 Ser Glu Lys Ala Ile His Pro Gln Tyr Leu Ala Gln Gln Ile Ser His
283          355         360         365
286 Phe Ala Ala Asp Asp Ala Ile Phe Thr Cys Asp Val Gly Thr Pro Thr
287          370         375         380
290 Val Trp Ala Ala Arg Tyr Leu Lys Met Asn Gly Lys Arg Arg Leu Leu
291 385         390         395         400
294 Gly Ser Phe Asn His Gly Ser Met Ala Asn Ala Met Pro Gln Ala Leu

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295          405          410          415
298 Gly Ala Gln Ala Thr Glu Pro Glu Arg Gln Val Val Ala Met Cys Gly
299          420          425          430
302 Asp Gly Gly Phe Ser Met Leu Met Gly Asp Phe Leu Ser Val Val Gln
303          435          440          445
306 Met Lys Leu Pro Val Lys Ile Val Val Phe Asn Asn Ser Val Leu Gly
307          450          455          460
310 Phe Val Ala Met Glu Met Lys Ala Gly Gly Tyr Leu Thr Asp Gly Thr
311 465          470          475          480
314 Glu Leu His Asp Thr Asn Phe Ala Arg Ile Ala Glu Ala Cys Gly Ile
315          485          490          495
318 Thr Gly Ile Arg Val Glu Lys Ala Ser Glu Val Asp Glu Ala Leu Gln
319          500          505          510
322 Arg Ala Phe Ser Ile Asp Gly Pro Val Leu Val Asp Val Val Val Ala
323          515          520          525
326 Lys Glu Glu Leu Ala Ile Pro Pro Gln Ile Lys Leu Glu Gln Ala Lys
327          530          535          540
330 Gly Phe Ser Leu Tyr Met Leu Arg Ala Ile Ile Ser Gly Arg Gly Asp
331 545          550          555          560
334 Glu Val Ile Glu Leu Ala Lys Thr Asn Trp Leu Arg
335          565          570
338 <210> SEQ ID NO: 3
339 <211> LENGTH: 1454
340 <212> TYPE: DNA
341 <213> ORGANISM: Escherichia coli
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344 <221> NAME/KEY: misc_feature
345 <222> LOCATION: (1)..(1454)
346 <223> OTHER INFORMATION: mutagenic DNA
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351 <222> LOCATION: (1)..(56)
352 <223> OTHER INFORMATION: technical DNA/residue of the polylinker sequence
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (57)..(577)
358 <223> OTHER INFORMATION: part of the 5' region (poxB1) of the poxB gene
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362 <221> NAME/KEY: misc_feature
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369 <222> LOCATION: (647)..(1398)
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374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (1399)..(1454)
376 <223> OTHER INFORMATION: technical DNA/residue of the polylinker sequence

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VERIFICATION SUMMARY

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DATE: 06/20/2002

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